



SEQUENCE LISTING

<110> Choe, Sunghwa
Feldmann, Kenneth A

<120> Dwf7 MUTANTS

<130> 2225-0003

<140> 09/775,879
<141> 2001-02-02

<150> 60/179,901
<151> 2000-02-02

<160> 25

<170> PatentIn Ver. 2.0

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer S5D_FF

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25

<210> 2
<211> 26
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer S5D_LR

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ggaaagatca tcaaacattt acatgt

26

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer S5D_1F

<400> 3
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19

<210> 4
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer S5D_1R

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tggacaacaa caacacaaga

20

<210> 5
<211> 22
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<223> Description of Artificial Sequence: Primer S5D_2F

<400> 5
gatgcacaga gagcttcatg ac

22

<210> 6
<211> 22
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer S5D_2R

<400> 6
ccggcaaattg gagagagtgt at

22

<210> 7
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer S5D_3F

<400> 7
cacccatcat atctacaaca a

21

<210> 8
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer S5D_4F

<400> 8
catcttttgc cggcgaatct at

22

<210> 9

<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer D7-5-1

<400> 9
gtagaagcac cagaggaaac cggagatgaa gt

32

<210> 10
<211> 26
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer D7-5-2

<400> 10
aagtatagtta gggttccggc gaggtt

26

<210> 11
<211> 26
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer D7-5-3

<400> 11
atagatttcgc cggcaaaaga tgactc

26

<210> 12
<211> 32
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer D7-3-1

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tgcaggatac catacgatac accacacgac at

32

<210> 13
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<212> DNA
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<223> Description of Artificial Sequence: Primer D7-3-2

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer D7-3-3

<400> 14
atatggatgg attggatgtt tggctctc

28

<210> 15
<211> 364
<212> PRT
<213> delta-7 sterol C-5 desaturase (Candida glabrata)

<400> 15
Met Asp Leu Val Leu Glu Thr Leu Asp His Tyr Ile Phe Asp Asp Val
1 5 10 15

Tyr Ala Lys Ile Ala Pro Val Glu Leu Gln Arg Gly Ile Asp Asp Ser
20 25 30

Leu Val Asn Ala Leu Ser Leu Asn Lys Ile Val Ser Asn Ser Thr Leu
35 40 45

Leu His Glu Thr Leu Ser Ile Thr Asn Ser Leu Lys Arg Val Asn Lys
50 55 60

Asp Val Tyr Gly Leu Thr Pro Phe Leu Phe Asp Phe Thr Glu Lys Thr
65 70 75 80

Tyr Ala Ser Leu Leu Pro Arg Asn Asn Leu Ile Arg Glu Phe Phe Ser
85 90 95

Leu Trp Ala Val Val Thr Val Phe Gly Leu Leu Leu Tyr Leu Ile Thr
100 105 110

Ala Ser Leu Ser Tyr Val Phe Val Phe Asp Arg Thr Ile Phe Asn His
115 120 125

Pro Lys Tyr Leu Lys Asn Gln Met Tyr Leu Glu Ile Lys Leu Ala Val
130 135 140

Ser Ala Ile Pro Thr Met Ser Leu Leu Thr Val Pro Trp Phe Met Leu
145 150 155 160

Glu Leu Asn Gly Tyr Ser Lys Leu Tyr Tyr Asp Val Asp Trp Glu His
165 170 175

His Gly Leu Arg Lys Leu Leu Ile Glu Tyr Ala Thr Phe Ile Phe Phe
180 185 190

Thr Asp Cys Gly Ile Tyr Leu Ala His Arg Trp Leu His Trp Pro Arg

195

200

205

Val Tyr Lys Ala Leu His Lys Pro His His Lys Trp Leu Val Cys Thr
210 215 220

Pro Phe Ala Ser His Ala Phe His Pro Val Asp Gly Tyr Phe Gln Ser
225 230 235 240

Leu Ser Tyr His Ile Tyr Pro Met Ile Leu Pro Leu His Lys Ile Ser
245 250 255

Tyr Leu Ile Leu Phe Thr Phe Val Asn Phe Trp Ser Val Met Ile His
260 265 270

Asp Gly Gln His Met Ser Asn Asn Pro Val Val Asn Gly Thr Ala Cys
275 280 285

His Thr Val His His Leu Tyr Phe Asn Tyr Asn Tyr Gly Gln Phe Thr
290 295 300

Thr Leu Trp Asp Arg Leu Gly Gly Ser Tyr Arg Arg Pro Glu Asp Ser
305 310 315 320

Leu Phe Asp Pro Lys Leu Lys Met Asp Lys Lys Val Leu Glu Lys Gln
325 330 335

Ala Arg Glu Thr Ala Ala Tyr Ile Gln Glu Val Glu Gly Asp Asp Thr
340 345 350

Asp Arg Val Tyr Asn Thr Asp Lys Lys Lys Thr Asn
355 360

<210> 16

<211> 365

<212> PRT

<213> delta-7 sterol C-5 desaturase (Saccharomyces cerevisiae)

<400> 16

Met Asp Leu Val Leu Glu Val Ala Asp His Tyr Val Leu Asp Asp Leu
1 5 10 15

Tyr Ala Lys Val Leu Pro Ala Ser Leu Ala Ala Asn Ile Pro Val Lys
20 25 30

Trp Gln Lys Leu Leu Gly Leu Asn Ser Gly Phe Ser Asn Ser Thr Ile
35 40 45

Leu Gln Glu Thr Leu Asn Ser Lys Asn Ala Val Lys Glu Cys Arg Arg
50 55 60

Phe Tyr Gly Gln Val Pro Phe Leu Phe Asp Met Ser Thr Thr Ser Phe
65 70 75 80

Ala Ser Leu Leu Pro Arg Ser Ser Ile Leu Arg Glu Phe Leu Ser Leu
85 90 95

Trp Val Ile Val Thr Ile Phe Gly Leu Leu Leu Tyr Leu Phe Thr Ala
100 105 110

Ser Leu Ser Tyr Val Phe Val Phe Asp Lys Ser Ile Phe Asn His Pro
115 120 125

Arg Tyr Leu Lys Asn Gln Met Ala Met Glu Ile Lys Leu Ala Val Ser
130 135 140

Ala Ile Pro Trp Met Ser Met Leu Thr Val Pro Trp Phe Val Met Glu
145 150 155 160

Leu Asn Gly His Ser Lys Leu Tyr Met Lys Ile Asp Tyr Glu Asn His
165 170 175

Gly Val Arg Lys Leu Ile Ile Glu Tyr Phe Thr Phe Ile Phe Phe Thr
180 185 190

Asp Cys Gly Val Tyr Leu Ala His Arg Trp Leu His Trp Pro Arg Val
195 200 205

Tyr Arg Ala Leu His Lys Pro His His Lys Trp Leu Val Cys Thr Pro
210 215 220

Phe Ala Ser His Ser Phe His Pro Val Asp Gly Phe Leu Gln Ser Ile
225 230 235 240

Ser Tyr His Ile Tyr Pro Leu Ile Leu Pro Leu His Lys Val Ser Tyr
245 250 255

Leu Ile Leu Phe Thr Phe Val Asn Phe Trp Thr Val Met Ile His Asp
260 265 270

Gly Gln Tyr Leu Ser Asn Asn Pro Ala Val Asn Gly Thr Ala Cys His
275 280 285

Thr Val His His Leu Tyr Phe Asn Tyr Asn Tyr Gly Gln Phe Thr Thr
290 295 300

Leu Trp Asp Arg Leu Gly Gly Ser Tyr Arg Arg Pro Asp Asp Ser Leu
305 310 315 320

Phe Asp Pro Lys Leu Arg Asp Ala Lys Glu Thr Trp Asp Ala Gln Val
325 330 335

Lys Glu Val Glu His Phe Ile Lys Glu Val Glu Gly Asp Asp Asn Asp
340 345 350

Arg Ile Tyr Glu Asn Asp Pro Asn Thr Lys Lys Asn Asn
355 360 365

<210> 17
<211> 329
<212> PRT
<213> delta-7 sterol C-5 desaturase (Schizosaccharomyces pombe)

<400> 17

Met Asp Val Val Leu Gln Tyr Ala Asp Lys Tyr Val Phe Asp Thr Phe
1 5 10 15

Tyr Gly Lys Ile Ala Glu Ser Phe Asp Ser Ser Ser Phe Ala Asn
20 25 30

Thr Ala Val Asn Ser Thr Thr Leu Gly Leu Ala Glu Lys Val Asn Phe
35 40 45

Ala Ile Thr Ser Gly Leu Leu Asp Arg Asn Asn Val Trp Arg Gln Phe
50 55 60

Thr Ser Leu Phe Leu Ile Thr Trp Ile Met Gly Thr Leu Ser Tyr Phe
65 70 75 80

Leu Ser Ala Ser Phe Ala Tyr Tyr Val Tyr Phe Asp Arg Glu Glu Ala
85 90 95

Arg Arg His Pro Lys Phe Leu Lys Asn Gln Glu His Leu Glu Leu Met
100 105 110

Val Ala Leu Lys Asn Leu Pro Gly Met Ala Ile Leu Thr Ala Pro Trp
115 120 125

Phe Leu Ala Glu Ile Arg Gly Tyr Gly Tyr Val Tyr Asp Lys Leu Asp
130 135 140

Glu Tyr Gly Tyr Phe Tyr Leu Phe Phe Ser Ile Ala Leu Phe Leu Leu
145 150 155 160

Phe Ser Asp Phe Leu Ile Tyr Trp Ile His Arg Ala Leu His His Arg
165 170 175

Trp Leu Tyr Ala Pro Leu His Lys Leu His His Lys Trp Ile Val Pro
180 185 190

Thr Pro Tyr Ser Ser His Ala Phe His Tyr Leu Asp Gly Tyr Ser Gln
195 200 205

Ser Leu Pro Tyr His Met Phe Pro Phe Phe Pro Leu Asn Lys Tyr
210 215 220

Val Tyr Leu Leu Leu Phe Gly Ser Val Asn Tyr Trp Thr Val Leu Ile
225 230 235 240

His Asp Gly Lys Tyr Phe Ser Asn Asn Ala Val Val Asn Gly Ala Ala
245 250 255

His His Ala Ala His His Met Tyr Phe Asn Tyr Asn Tyr Gly Gln Phe
260 265 270

Phe Thr Leu Phe Asp Arg Leu Cys Ser Ser Tyr Arg Gln Pro Asp Gln
275 280 285

Glu Leu Phe Asp Ala Glu Leu Arg Asn Glu Lys Leu Gln Glu Gln Arg
290 295 300

Ile Arg Phe Met Glu Thr Val Gln Tyr Thr Val Glu Gly Lys Asp Asp
305 310 315 320

Arg Thr Tyr Ala Ser Lys Lys Asp Asn
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<210> 18

<211> 281

<212> PRT

<213> DWF7/STE1 (Arabidopsis)

<400> 18

Met Ala Ala Asp Asn Ala Tyr Leu Met Gln Phe Val Asp Glu Thr Ser
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Phe Tyr Asn Arg Ile Val Leu Ser His Leu Leu Pro Ala Asn Leu Trp
20 25 30

Glu Pro Leu Pro His Phe Leu Gln Thr Trp Leu Arg Asn Tyr Leu Ala
35 40 45

Gly Thr Leu Leu Tyr Phe Ile Ser Gly Phe Leu Trp Cys Phe Tyr Ile
50 55 60

Tyr Tyr Leu Lys Ile Asn Val Tyr Leu Pro Lys Asp Ala Ile Pro Thr
65 70 75 80

Ile Lys Ala Met Arg Leu Gln Met Phe Val Ala Met Lys Ala Met Pro
85 90 95

Trp Tyr Thr Leu Leu Pro Thr Val Ser Glu Ser Met Ile Glu Arg Gly
100 105 110

Trp Thr Lys Cys Phe Ala Ser Ile Asp Glu Phe Gly Trp Ile Leu Tyr
115 120 125

Phe Val Tyr Ile Ala Ile Tyr Leu Val Phe Val Glu Phe Gly Ile Tyr
130 135 140

Trp Met His Arg Glu Leu His Asp Ile Lys Pro Leu Tyr Lys Tyr Leu
145 150 155 160

His Ala Thr His His Ile Tyr Asn Lys Gln Asn Thr Leu Ser Pro Phe
165 170 175

Ala Gly Leu Ala Phe His Pro Val Asp Gly Ile Leu Gln Ala Val Pro
180 185 190

His Val Ile Ala Leu Phe Ile Val Pro Ile His Phe Thr Thr His Ile
195 200 205

Gly Leu Leu Phe Met Glu Ala Ile Trp Thr Ala Asn Ile His Asp Cys
210 215 220

Ile His Gly Asn Ile Trp Pro Val Met Gly Ala Gly Tyr His Thr Ile
225 230 235 240

His His Thr Thr Tyr Lys His Asn Tyr Gly His Tyr Thr Ile Trp Met
245 250 255

Asp Trp Met Phe Gly Ser Leu Arg Asp Pro Leu Leu Glu Glu Asp Asp
260 265 270

Asn Lys Asp Ser Phe Lys Lys Ala Glu
275 280

<210> 19
<211> 291
<212> PRT
<213> delta-7 sterol C-5 desaturase concensus

<400> 19
Met Asp Leu Val Leu Glu Ala Asp His Tyr Val Phe Asp Asp Tyr Ala
1 5 10 15

Lys Ile Pro Leu Ala Ile Asp Ser Leu Leu Asn Val Ser Asn Ser Thr
20 25 30

Leu Glu Thr Leu Asn Lys Val Asn Tyr Gly Pro Phe Leu Phe Asp Phe
35 40 45

Thr Glu Thr Ser Phe Ser Leu Leu Pro Arg Asn Asn Leu Trp Arg Glu
50 55 60

Phe Leu Ser Leu Trp Leu Ile Val Thr Ile Phe Gly Leu Leu Tyr Ile
65 70 75 80

Ala Ser Leu Ser Tyr Phe Phe Asp Ile Phe Asn His Pro Lys Tyr Leu
85 90 95

Lys Asn Gln Met Leu Glu Ile Lys Ala Val Ala Ile Pro Trp Met Ser
100 105 110

Leu Leu Thr Val Pro Trp Phe Met Glu Leu Gly Tyr Ser Lys Leu Tyr
115 120 125

Tys Ile Asp Glu His Gly Arg Iys Leu Phe Ile Glu Ala Thr Phe Phe
130 135 140

Phe Thr Asp Gly Ile Tyr Ala His Arg Trp Leu His Trp Pro Tyr Lys
145 150 155 160

Ala Leu His Lys Pro His His Lys Trp Leu Val Cys Thr Pro Phe Ala
165 170 175

Ser His Ala Phe His Pro Val Asp Gly Tyr Leu Gln Ser Leu Tyr His
180 185 190

Ile Tyr Pro Leu Leu Pro Leu His Lys Ser Tyr Leu Leu Phe Thr Phe
195 200 205

Val Asn Phe Trp Thr Val Met Ile His Asp Gly Gln Ser Asn Asn Pro
210 215 220

Val Val Asn Gly Ala Cys His Thr Val His His Leu Tyr Phe Asn Tyr
225 230 235 240

Asn Tyr Gly Gln Phe Thr Thr Leu Trp Asp Arg Leu Gly Gly Ser Tyr
245 250 255

Arg Arg Pro Asp Ser Leu Phe Asp Pro Lys Leu Arg Asp Lys Lys Glu
260 265 270

Gln Arg Glu Thr Tyr Ile Glu Val Glu Gly Asp Asp Asp Arg Tyr Asp
275 280 285

Lys Lys Asn
290

<210> 20

<211> 1889

<212> DNA

<213> Genomic *dwf7* (*Arabidopsis*)

<400> 20

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tctcgggtga tctccgattc acatggcgcc ggataatgct tatctgatgc agtttggta 180
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aaaacatgtta aatgtttgat gatctttgc 1889

<210> 21
<211> 281
<212> PRT
<213> DWF7

<400> 21
Met Ala Ala Asp Asn Ala Tyr Leu Met Gln Phe Val Asp Glu Thr Ser
1 5 10 15

Phe Tyr Asn Arg Ile Val Leu Ser His Leu Leu Pro Ala Asn Leu Trp
20 25 30

Glu Pro Leu Pro His Phe Leu Gln Thr Trp Leu Arg Asn Tyr Leu Ala
35 40 45

Gly Thr Leu Leu Tyr Phe Ile Ser Gly Phe Leu Trp Cys Phe Tyr Ile
50 55 60

Tyr Tyr Leu Lys Ile Asn Val Tyr Leu Pro Lys Asp Ala Ile Pro Thr
65 70 75 80

Ile Lys Ala Met Arg Leu Gln Met Phe Val Ala Met Lys Ala Met Pro
85 90 95

Trp Tyr Thr Leu Leu Pro Thr Val Ser Glu Ser Met Ile Glu Arg Gly
100 105 110

Trp Thr Lys Cys Phe Ala Ser Ile Asp Glu Phe Gly Trp Ile Leu Tyr
115 120 125

Phe Val Tyr Ile Ala Ile Tyr Leu Val Phe Val Glu Phe Gly Ile Tyr
130 135 140

Trp Met His Arg Glu Leu His Asp Ile Lys Pro Leu Tyr Lys Tyr Leu
145 150 155 160

His Ala Thr His His Ile Tyr Asn Lys Gln Asn Thr Leu Ser Pro Phe
165 170 175

Ala Gly Leu Ala Phe His Pro Val Asp Gly Ile Leu Gln Ala Val Pro
180 185 190

His Val Ile Ala Leu Phe Ile Val Pro Ile His Phe Thr Thr His Ile
195 200 205

Gly Leu Leu Phe Met Glu Ala Ile Trp Thr Ala Asn Ile His Asp Cys
210 215 220

Ile His Gly Asn Ile Trp Pro Val Met Gly Ala Gly Tyr His Thr Ile
225 230 235 240

His His Thr Thr Tyr Lys His Asn Tyr Gly His Tyr Thr Ile Trp Met
245 250 255

Asp Trp Met Phe Gly Ser Leu Arg Asp Pro Leu Leu Glu Glu Asp Asp
260 265 270

Asn Lys Asp Ser Phe Lys Lys Ala Glu
275 280

<210> 22

<211> 2925

<212> DNA

<213> Genomic HDF7

<400> 22

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<210> 23

<211> 279

<212> PRT

<213> HDF7

<400> 23

Met Ala Ala Thr Met Ala Asp Tyr Asn Asp Gln Ile Val Asn Glu Thr
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Ser Phe Tyr Asn Arg Met Val Leu Ser His Leu Leu Pro Val Asn Leu
20 25 30

Trp Glu Pro Leu Pro His Phe Leu Gln Thr Trp Leu Arg Asn Tyr Leu
35 40 45

Ala Gly Asn Ile Leu Tyr Phe Ile Ser Gly Phe Leu Trp Cys Phe Tyr
50 55 60

Ile Tyr Tyr Leu Lys Leu Asn Val Tyr Val Pro Lys Glu Ser Ile Pro
65 70 75 80

Thr Arg Lys Ala Met Leu Leu Gln Ile Tyr Val Ala Met Lys Ala Met
85 90 95

Pro Trp Tyr Thr Leu Leu Pro Ala Val Ser Glu Tyr Met Ile Glu His
100 105 110

Gly Trp Thr Lys Cys Tyr Ser Thr Leu Asp His Phe Asn Trp Phe Leu
115 120 125

Cys Phe Leu Tyr Ile Ala Leu Tyr Leu Val Leu Val Glu Phe Met Ile
130 135 140

Tyr Trp Val His Lys Glu Leu His Asp Ile Lys Phe Leu Tyr Lys His
145 150 155 160

Leu His Ala Thr His His Met Tyr Asn Lys Gln Asn Thr Leu Ser Pro
165 170 175

Phe Ala Gly Leu Ala Phe His Pro Leu Asp Gly Ile Leu Gln Ala Ile
180 185 190

Pro His Val Ile Ala Leu Phe Ile Val Pro Ile His Leu Ile Thr His
195 200 205

Leu Ser Leu Leu Phe Leu Glu Gly Ile Trp Thr Ala Ser Ile His Asp
210 215 220

Cys Ile His Gly Asn Ile Trp Pro Ile Met Gly Ala Gly Tyr His Thr
225 230 235 240

Ile His His Thr Thr Tyr Lys His Asn Tyr Gly His Tyr Thr Ile Trp
245 250 255

Met Asp Trp Met Phe Gly Ser Leu Met Val Pro Leu Ala Glu Lys Asp
260 265 270

Ser Phe Lys Glu Lys Glu Lys
275

<210> 24

<211> 60

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Met Ala Ala Asp Asn Ala Tyr Leu Met Gln Phe Val Asp Glu Thr Ser
1 5 10 15

Phe Tyr Asn Arg Ile Val Leu Ser His Leu Leu Pro Ala Asn Leu Trp
20 25 30

Glu Pro Leu Pro His Phe Leu Gln Thr Trp Leu Arg Asn Tyr Leu Ala
35 40 45

Gly Thr Leu Leu Tyr Phe Ile Ser Gly Phe Leu Trp
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1 5 10 15

Phe Tyr Asn Arg Ile Val Leu Ser His Leu Leu Pro Ala Asn Leu Trp
20 25 30

Glu Pro Leu Pro His Phe Leu Gln Thr Trp Leu Arg Asn Tyr Leu Ala
35 40 45

Gly Thr Leu Leu Tyr Phe Ile Ser Gly Phe Leu Trp Cys Phe Tyr Ile
50 55 60

Tyr Tyr Leu Lys Ile Asn Val Tyr Leu Pro Lys Asp Ala Ile Pro Thr
65 70 75 80

Ile Lys Ala Met Arg Leu Gln Met Phe Val Ala Met Lys Ala Met Pro
85 90 95

Trp Tyr Thr Leu Leu Pro Thr Val Ser Glu Ser Met Ile Glu Arg Gly
100 105 110

Trp Thr Lys Cys Phe Ala Ser Ile Asp Glu Phe Gly Trp Ile Leu Tyr
115 120 125

Phe Val Tyr Ile Ala Ile Tyr Leu Val Phe Val Glu Phe Gly Ile Tyr
130 135 140

Trp Met His Arg Glu Leu His Asp Ile Lys Pro Leu Tyr Lys Tyr Leu
145 150 155 160

His Ala Thr His His Ile Tyr Asn Lys Gln Asn Thr Leu Ser Pro Phe
165 170 175

Ala Gly Leu Ala Phe His Pro Val Asp Gly Ile Leu Gln Ala Val Pro
180 185 190

His Val Ile Ala Leu Phe Ile Val Pro Ile His Phe Thr Thr His Ile
195 200 205

Gly Leu Leu Phe Met Glu Ala Ile Trp Thr Ala Asn Ile His Asp Cys
210 215 220

Ile His Gly Asn Ile Trp
225 230